WHAT WE CLAIM IS:

1. An isolated nucleic acid molecule of a sheep type of *M. paratuberculosis* said molecule comprising SEQ ID NO. 1 or a complement thereof.

2. A probe comprising SEQ ID NO.1 or a complement thereof.

3. A probe comprising at least 20 or more contiguous nucleotides selected from nucleotides 230 – 260 of SEQ ID NO. 1 or a complement thereof.

4. The use of a nucleic acid molecule or probe as claimed in any one of claims 1-3 for detecting the presence of sheep types of *M. paratuberculosis*.

5. The use of SEQ ID NO 2 or, a fragment or complement thereof for detecting the presence of cattle types of *M. paratuberculosis*.

6. A method of distinguishing between cattle and sheep types of *M. paratuberculosis* comprising the step of comparing differences between the nucleotide sequences of SEQ ID NO. 1 and SEQ ID NO. 2 or complements of said sequences.

7. A method of detecting the presence of *M. paratuberculosis* in a sample via a nucleic acid amplification technique said method comprising the steps of:

   a) taking a sample from an animal or any other source;

   b) extracting nucleic acids from the sample or culturing mycobacteria from the sample and extracting nucleic acids from the mycobacterial culture;

c) performing a nucleic acid amplification technique with one or more nucleic acid sequences as claimed in claim 1; and

d) determining the identity of the amplification product.

8. A method as claimed in claim 7 wherein the animals may include cattle, sheep, deer, goats, ferrets, rabbits and humans.

9. A method as claimed in claim 7 wherein step d) of the method comprises identifying the presence of 10-12 contiguous nucleotides of the nucleic acid molecule comprising SEQ ID NO. 1 or a complement thereof.

10. A method claimed in claim 7 wherein step d) of the method comprises identifying the presence of at least 15 contiguous nucleotides of the nucleic acid molecule comprising SEQ ID NO. 1 or a complement thereof.

11. A method as claimed in claim 7 wherein step d) of the method comprises identifying the presence of substantially 20 contiguous nucleotides of the nucleic acid molecule comprising SEQ ID NO. 1 or a complement thereof.

12. A method as claimed in claim 7 step c) utilizes one oligonucleotide primer complementary to 10-12 contiguous nucleotides of SEQ ID NO. 1 or a complement thereof; and one oligonucleotide primer complementary to 10-12 nucleotides of IS*900* or a complement thereof.

13. A method as claimed in claim 7 wherein step c) utilizes one oligonucleotide primer complementary to substantially 15 contiguous nucleotides of SEQ ID NO. 1 or a complement thereof; and one oligonucleotide primer complementary to substantially 15 nucleotides of IS*900* or a complement thereof.

14. A method as claimed in claim 7 wherein step c) utilizes one oligonucleotide primer complementary to substantially 20 contiguous nucleotides of SEQ ID NO. 1 or a complement thereof; and one oligonucleotide primer complementary to substantially 20 nucleotides of IS*900* or a complement thereof.

15. A method as claimed in claim 7 wherein step d) of the method comprises identifying the presence of 10-12 contiguous nucleotides of the nucleic acid molecule comprising SEQ ID NO. 2 or a complement thereof.

16. A method as claimed in claim 7 wherein step d) of the method comprises identifying the presence of at least 15 contiguous nucleotides of the nucleic acid molecule comprising SEQ ID NO. 2 or a complement thereof.

17. A method as claimed in claim 7 wherein step d) of the method comprises identifying the presence of approximately 20 contiguous nucleotides of the nucleic acid molecule comprising SEQ ID NO. 2 or a complement thereof.

18. A method as claimed in claim 7 wherein step c) utilizes one oligonucleotide primer complementary to 12 contiguous nucleotides of SEQ ID NO. 2 or a complement thereof; and one oligonucleotide primer complementary to 10-12 nucleotides of IS*900* or a complement thereof.

19. A method as claimed in claim 7 wherein step c) utilizes one oligonucleotide primer complementary to substantially 15 contiguous nucleotides of SEQ ID NO. 2 or a complement thereof; and one oligonucleotide primer complementary to substantially 15 nucleotides of IS*900* or a complement thereof.

20. A method as claimed in claim 7 wherein step c) utilizes one oligonucleotide primer complementary to substantially 20 contiguous

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nucleotides of SEQ ID NO. 2 or a complement thereof; and one oligonucleotide primer complementary to substantially 20 contiguous nucleotides of IS*900* or a complement thereof.

21. The use of a probe comprising substantially 10-12 contiguous nucleotides selected from the nucleic acid comprising SEQ ID NO. 2 or a complement thereof to determine whether a strain of either sheep type or cattle type *M. paratuberculosis* is present in a sample.

22. The use of a probe comprising at least 15 contiguous nucleotides selected from the nucleic acid comprising SEQ ID NO. 2 or a complement thereof to determine whether a strain of either sheep type or cattle type *M. paratuberculosis* is present in a sample.

23. The use of a probe comprising at least 20 contiguous nucleotides selected from the nucleic acid comprising SEQ ID NO. 2 or a complement thereof to determine whether a strain of either sheep type or cattle type *M. paratuberculosis* is present in a sample.

24. The use of SEQ ID NO.1 and/or SEQ ID NO. 2, or a fragment or complement thereof, to determine whether a strain of either a sheep type or a cattle type of *M. paratuberculosis* is present in a sample.

25. The use of SEQ ID NO.1, or a fragment or complement thereof, to distinguish any strain of *M. paratuberculosis* from any other strain of the MAI complex which may be present in a sample.

26. The use of SEQ ID NO.2, or a fragment or complement thereof, to distinguish any strain of *M. paratuberculosis* from any other strain of the MAI complex which may be present in a sample.

27. The use of SEQ ID NO.1, or a fragment or complement thereof, to distinguish any strain of *M. paratuberculosis* from any strain of the *M. tuberculosis* complex which may be present in a sample.

28. The use of SEQ ID NO.2, or a fragment or complement thereof, to distinguish any strain of *M. paratuberculosis* from any strain of the *M. tuberculosis* complex which may be present in a sample.

29. The use of SEQ ID NO. 1, or a fragment or complement thereof, to detect the presence of *M. paratuberculosis* as a causative agent of Johne's disease or Crohn's disease.

30. The use of SEQ ID NO. 2, or a fragment or complement thereof, to detect the presence of *M. paratuberculosis* as a causative agent of Johne's disease or Crohn's disease.